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 Copyright (c) 1993 - 2000 Compugen Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: May 24, 2002, 19:15:39 ; Search time 1997.16 Seconds
 (without alignments)
 3981.696 Million cell updates/sec

Title:

Perfect score:

Sequence:

Scoring table:

Searched:

Post-processing:

Total number of hits satisfying chosen parameters:

Minimum DB seq length:

Maximum DB seq length:

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| FEATURE | REFERENCE | ORGANISM | SOURCE |
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| REFERENCE | 3 (bases 1 to 2347) | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | |
| AUTHORS | Krieg, P., Siebert, M., Kinzig, A., Marks, F. and Fuerstenberger, G. | | |
| TITLE | Murine 12(R)-lipoxygenase: functional expression, genomic structure and chromosomal localization | | |
| JOURNAL | Unpublished | | |
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| | SHPRBRCRNPRNPRDGYTFLPLINRQKTRAKTASFPYRIGPQ | | |
| | LAFKLRQDVRKRSWRKDKNIFKATSVSEVAEHTEDSFPGYQYLNGINPL | | |
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| | HARVAKLLESHLIGEAFCLALRNLMPIKLUFLITKYNQINSIGRALLNKG | | |
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| ORIGIN | | | |
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| Best Local Similarity | 98.5% | Pred. No. 1.9e-36; 0; Mismatches 2; Indels 1; Gaps 1; | |
| Matches | 199; Conservative | | |
| Db | 175 TTCCCTGGCCCTAGAGGCTCTGCAACAGACTTGTGGAGCGGGGGTCCAGGACCTGCCGGT 234 | | |
| Db | 1542 TGTCCCTGGCCCTAGAGGCTCTGCAACAGACTTGTGGAGCGGGGGTCCAGGACCTGCCGGT 1601 | | |
| Db | 235 ACAAAAGCCCTGATCCAAAGACTTGTGGAGCGGGGGTCCAGGACCTGCCGGT 294 | | |
| Db | 1602 ACAAAAGCCCTGATCCAAAGACTTGTGGAGCGGGGGTCCAGGACCTGCCGGT 1661 | | |
| Db | 295 ATTATTCGGTGTGACAGCCTGCGGGTGGAGGAGGTACGGTACAGTAGAG 354 | | |
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| Db | 355 ATCATCACTTATTACCAA 376 | | |
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| AFO5251 | LCUC5 AF059251 | 2225 bp mRNA linear | ROD 27-Nov-1998 |
| DEFINITION | Mus musculus lipoxygenase (alox) mRNA, complete cds. | | |
| ACCESSION | AF059251 | | |
| VERSION | AF059251.1 | GI:328784 | |
| KEYWORDS | | | |

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| RESULT | AL645527 | 4 |
| LOCUS | | |
| DEFINITION | Mus musculus chromosome 11 clone RP23-26L6, *** | SEQUENCING IN |
| ACCESSION | AL645527 | |
| VERSION | AL645527.12 | |
| KEYWORDS | HGNC; HGVS_PBSAF1; HGVS_ACTIVEF1N; HGVS_DRAFT; HGVS_FULLTOP | |
| SOURCE | | |
| ORGANISM | Mus musculus | |
| | house mouse. | |
| REFERENCE | AL645527 | |
| JOURNAL | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (sities) | |
| AUTHORS | Ashwell, R. | |
| TITLE | Direct Submission | |
| | Submitted (23-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquer@esanger.ac.uk Clone requests: clonerequest@sanger.ac.uk | |
| COMMENT | On Jan 19, 2002 this sequence version replaced g1:18152591. | |
| | ----- Genome Center | |

Query Match 43.8%; Score 166.4; DB 2; Length 261031; ORIGIN

Best Local Similarity 99.4%; Pred. No. 1.e-31; Mismatches 0; Indels 1; Gaps 0; Matches 167; Conservative

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Db 82649 TGTCCCTGGCCCTAGAGGCTCGACAGGTGATGGTCTGGGGCTGCTCTGAGCTCACCT 82708

QY 235 ACAAAAGCCTCTGATGCCAACGACTTGTGGAGCCGGGGTCCAGGACCTGCCCTGGT 294
Db 82709 ACAAAAGCCTCTGATGCCAACGACTTGTGGAGCCGGGGTCCAGGACCTGCCCTGGT 82768

QY 295 ATTATTTCGGTGTGACAGCAGCCGGCTGCTACCGATGGAGGT 342
Db 82769 ATTATTTCGGTGTGACAGCAGCCGGCTGCTACCGATGGAGGT 82816

RESULT 5

AF059250 AF059250 AF059250.1 LOCUS mRNA DEFINITION Homo sapiens lipoxygenase (ALOX12B) mRNA, complete cds. ACCESSION AR059250 VERSION GI:39287822 KEYWORDS human.

SOURCE ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2278) AUTHORS Sun, D., Mcbonell, M., Chen, X. S., Lakkis, M. M., Li, H., Isaacs, S. N., Elsea, S. H., Patel, P. R. and Funk, C. D.

TITLE Human 12(R)-lipoxygenase and the mouse ortholog. Molecular cloning, expression, and gene chromosomal assignment

JOURNAL J. Biol. Chem. 273 (50), 33540-33547 (1998)

MEDLINE 99057919

REFERENCE 2 (bases 1 to 2278) AUTHORS Sun, D. and Funk, C. D.

TITLE Direct submission

JOURNAL Submitted (13-APR-1998) Pharmacology, University of Pennsylvania, 422 Curie Blvd., Philadelphia, PA 19104, USA

FEATURES source

source

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38..2143

Query Match 35.7%; Score 135.8; DB 6; Length 2469; ORIGIN

Best Local Similarity 83.4%; Pred. No. 1.e-23; Mismatches 0; Indels 1; Gaps 1; Matches 166; Conservative

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BASE COUNT 510 a 720 c 596 g 452 t

ORIGIN

Query Match 35.7%; Score 135.8; DB 9; Length 2278; ORIGIN

Best Local Similarity 83.4%; Pred. No. 1.e-23; Mismatches 0; Indels 1; Gaps 1; Matches 166; Conservative

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Db 1464 ATGACAGCCTCTACCTCCCAACTGACTTGTGGACGCCGGGCCAGGACCTCCCTGGT 1523

QY 295 ATTATTTCGGTGTGACAGCAGCCGGCTGCTACCGATGGAGGTACGACTAG 354
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RESULT 6

AR106047 LOCUS AR106047 DEFINITION Sequence 1 from patent US 6103496. DNA LINEAR PAT 14-FEB-2001

ACCESSION AR106047 VERSION AR106047.1 GI:12820112

KEYWORDS

SOURCE ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2469)

AUTHORS Brash, A. R., Boenigk, W. E. and Kim, R. B.

JOURNAL Isolated and purified 12R-lipoxygenase protein and nucleic acids Patent: US 6103496-A 1 15-AUG-2000; Location/Qualifiers

FEATURES source

1..2469

/organism="unknown"

BASE COUNT 522 a 808 c 648 g 491 t

ORIGIN

Query Match 35.7%; Score 135.8; DB 6; Length 2469; ORIGIN

Best Local Similarity 83.4%; Pred. No. 1.e-23; Mismatches 0; Indels 1; Gaps 1; Matches 166; Conservative

QY 175 TTTCCCTGGCCCTAGAGGCTCGACAGGTGATGGTCTGGGGCTGCTCTGAGCTCACCT 234
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| • AF038461 | | | RESULT | 8 | |
| LOCUS | AF038461 | 2469 bp mRNA linear PRI 16-JUN-1998 | LOCUS | HSA305027 | |
| DEFINITION | Homo sapiens | 12R-lipoxygenase mRNA, complete cds. | DEFINITION | HSA305027 | |
| ACCESSION | AF038461 | | ORGANISM | Homo sapiens | |
| VERSION | AF038461.1 | GI:3220165 | COMMENT | | |
| KEYWORDS | human. | | FEATURES | | |
| SOURCE | Homo sapiens | | source | | |
| REFERENCE | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | REFERENCE | | |
| AUTHORS | Boeglin, W.E., Kim, R.B. and Brash, A.R. | | AUTHORS | | |
| TITLE | A 12R-lipoxygenase in human skin: mechanistic evidence, molecular cloning, and expression | | TITLE | | |
| JOURNAL | Proc. Natl. Acad. Sci. U.S.A. 95 (12), 6744-6749 (1998) | | JOURNAL | | |
| MEDLINE | 98244002 | | REFERENCE | | |
| REFERENCE | 2 (bases 1 to 2469) | | AUTHORS | | |
| AUTHORS | Boeglin, W.E., Jisaka, M., Kim, R.B. and Brash, A.R. | | TITLE | | |
| TITLE | Direct Submission | | JOURNAL | | |
| JOURNAL | Submitted (14-DEC-1997) Clinical Pharmacology, Vanderbilt University, MBII R#510, 23rd Ave S, at Pierce, Nashville, TN 37232-6602, USA | | REFERENCE | | |
| FEATURES | Location/Qualifiers | | AUTHORS | | |
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| Best Local Similarity | 83.4% | Pred. No. 1e-23; | AUTHORS | | |
| Matches | 166; | Conservative 0; Mismatches 32; Indels 1; Gaps 1; | TITLE | | |
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QY 235 ACACAAAGCTCTGCAATTCCAAAGACTTGTGGAGCCGGGCTCCAGGACCTGCCCTGGT 294
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QY 295 ATTATTCGGTATGACGCCGCGCTGGTACCCGATGAGAGT 342
Db 7297 ATTACTACCGCGATGACGCTGGCGTGGATGCACTGGAGAATG 7344
RESULT 9
AC015734 AC015734 159582 bp DNA linear HMG 13-Nov-2001
LOCUS AC015734
DEFINITION Homo sapiens clone RP11-1D5, WORKING DRAFT SEQUENCE, 13 unordered
PIECES
ACCESSION AC015734
VERSION AC015734.4 GI:16905302

```

KEYWORDS HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 159582)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 159582)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguski,M., Collins,S., Collymore,A., Cooke,P., Dearlano,K., Dewar,K., Domino,M., Donlan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyne,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kahn,L., Karatas,A., Klein,J., Lebo茨ky,J., Lieu,C., Locke,K., Macdonald,P., Marcus,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., Morow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Wiman,D., Ye,W.J., Zimmer,A. and Zody,M.

JOURNAL Direct Submission

COMMENT Submitted (17-NOV-1998) Whitehead Institute/MIT Center for Genome Research, 330 Charles Street, Cambridge, MA 02141, USA

On Nov 13, 2001 this sequence version replaced 91:7543748. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Project Information

Center Project Name: L1433

Center Clone Name: L1_D_5

Summary

Sequencing vector: M13; M77815; 49% of reads

Sequencing vector: Plasmid; n/a; 51% of reads

Chemistry: Dye-terminator

Assembly program: Phrap; version 0.96031

Consensus quality: 155110 bases at least 040

Consensus quality: 15690 bases at least Q30

Consensus quality: 15788 bases at least Q20

Insert size: 119000; agarose-fp

Insert size: 158382; agarose-fp

Quality coverage: 10.7 in 020 bases; agarose-fp

Quality coverage: 8.1 in Q20 bas.

NOTE: This is a working draft sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1481 1480: contig of 1480 bp in length

1 1581 1580: gap of 100 bp

1 1581 1580: 2920: contig of 1340 bp in length

1 1581 1580: gap of 100 bp

1 1581 1580: 3020: gap of 3204 bp in length

1 1581 1580: 6324: gap of 100 bp

1 1581 1580: 13162: contig of 6838 bp in length

1 1581 1580: 13163 13262: gap of 100 bp

1 1581 1580: 13163 13152: contig of 5890 bp in length

1 1581 1580: 19153 19152: gap of 100 bp

1 1581 1580: 19252: gap of 100 bp

1 1581 1580: 19253 73123: contig of 54171 bp in length

1 1581 1580: 73124 73523: gap of 100 bp

1 1581 1580: 73124 81434: contig of 7911 bp in length

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FEATURES

source

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QY 175 TTTCCCTGGCCCTAGAGGCTTCACAGGTGAGGTTGGCTGAGCTACCT 234

DB 157766 TGTCCCTGGCTGGAGGCTTGTGGGTGATGCTGGCTGCTGGAGCTACCT 157825

QY 235 ACAAAAGCCCTCTGCAATTCCAAACACTTGTGAGGGGGTCCAGGACCTGGT 294

DB 157826 ATGACAGCCCTACCTCCCAATGACTGTTGGAGCTGGCTGGAGCTACCT 157885

QY 295 ATTAATTCGGTGGAGACGCTTGCAGGCTGGAGCTGGAGCTGGAGCTGGAT 342

DB 157886 ATTACATACCGCGATGACAGCTTGGGGTGTGGATGCACTGGAGAAGT 157933

RESULT 10

MNU18477 MMU18477

LCUS DEFINITION MUS *musculus* *Alox12B* gene 5, flanking region.

ACCESSION Y18477

VERSION Y18477.1 GI:4586204
 KEYWORDS 12(R)-lipoxygenase; Alox12B gene.
 SOURCE house mouse.
 ORGANISM Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
 REFERENCE 1. (bases 1 to 3626)
 AUTHORS Krieg,P., Sibbert,M., Kinzig,A., Bettenhausen,R., Marks,F. and Furstenberger,G.
 TITLE Murine 12(R)-lipoxygenase: functional expression, genomic structure and chromosomal localization
 JOURNAL FEBS Lett. 446 (1), 142-148 (1999)
 JOURNAL Research Program 2, Im Neuenheimer Feld 280, D-69120 Heidelberg, FRG
 JOURNAL Submitted (26-NOV-1998) P. Krieg, German Cancer Research Center, FRG
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 QY 63 TCCATCACTGACTCCATCACTCTCGCTGCTGGCTTCCGCTGACTGC 106
 DB 3501 TCCATCACTGACTCCATCACTCTCGCTTCCGCTGACTGC 3544
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 CDS Homo sapiens partial ALOXE3 gene for arachidonate lipoxygenase 3,
 DEFINITION exons 5 to 11.
 ACCESSION AJ305021.1 GI:13374915
 VERSION 1
 KEYWORDS ALOXE3 gene; arachidonate lipoxygenase 3.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Cetartiodactyla; Homidae; Homo.
 REFERENCE 1. (bases 1 to 4293)
 AUTHORS Krieg,P., Marks,F. and Furstenberger,G.
 TITLE A gene cluster encoding human epidermis-type lipoxygenases at chromosome 17p13.1: Cloning, physical mapping, and expression
 JOURNAL
 RELATED REFERENCES
 2 (bases 1 to 4293)
 AUTHORS Krieg,P.R.
 TITLE Direct Submission
 JOURNAL Submitted (18-AUG-2000) Krieg,P.R., Research Program on Tumor Cell Regulation, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 280, Heidelberg, D-69120, GERMANY
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 COMMENT AC015734.

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 Best Local Similarity 50.5%; Pred. No. 0.00035;

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 BASE COUNT ORIGIN
 676 a 996 c 769 g 641 t

| Query | Match | Score | DB | Length |
|-------|---|-------------|---------|-----------|
| QY | 14.5% Best Local Similarity 111; Conservative | 55.2; | 9; | 3082; |
| Db | 54.4%; Matches 0; MisMatches 93; | Pred. No. 0 | 0.0013; | Indels 0; |
| QY | 177 TCCCTGGCCTAGAGCTTCGACAGGTGATGTTGGGCTCTGCTGAGCTACACTAC | 236 | | |
| Db | 1600 TCCATCGGGAGCAAGGGCTCATCTACCTCAGGACGACGGCCCTGGCCACTTACACTAC | 1659 | | |
| QY | 237 AAAAGCTCTGAGTCCAAAGACTTGTGAGCCGGGACAGGACCCCTGGTAT | 296 | | |
| Db | 1660 ACCAATTCTGGCTTCGGACAGGCCGGGGCCGGCGGCGCTTGCTATCCCACTAC | 1719 | | |
| QY | 297 TATTTCCCTGATACAGCAGCTGGGGTGTGGTACCGATGGAGAGGTACGTACAGAT | 356 | | |
| Db | 1720 CACTACCGAGACCGGGCTGAGATGTGGGGCCATTGTGAGAGCTTGCTCAGAAC | 1779 | | |
| QY | 357 CACTACTTATTATACAAATAC | 380 | | |
| Db | 1780 GTGGCTACTATATCCAGTGAC | 1803 | | |

Search completed: May 25, 2002, 01:27:44
 Job time: 22325 sec

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|--|--|-------|--------|----|-----------|-------------|--|---|--|--|--|
| Copyright (c) 1993 - 2000 Compugen Ltd. | GenCore version 4.5 | | | | | | | | | | |
| OM nucleic - nucleic search, using sw model | | | | | | | | | | | |
| Run on: May 24, 2002, 18:05:53 ; Search time 1935.21 Seconds | (without alignments) | | | | | | | | | | |
| - Scoring table: IDENTITY NUC | 2650.277 Million cell updates/sec | | | | | | | | | | |
| Title: W36511 | | | | | | | | | | | |
| Perfect score: 380 | GCAGGCAGCAGCTGCRC... ACTTATTATTACCAAAATGAC 380 | | | | | | | | | | |
| Sequence: GCGAGCAGCAGCTGCRC... ACTTATTATTACCAAAATGAC 380 | | | | | | | | | | | |
| - Scoring table: Gapop 10.0 , Gapext 1.0 | | | | | | | | | | | |
| searched: 13736207 seqs, 6748477542 residues | | | | | | | | | | | |
| Total number of hits satisfying chosen parameters: 27472414 | | | | | | | | | | | |
| Minimum DB seq length: 0 | | | | | | | | | | | |
| Maximum DB seq length: 200000000 | | | | | | | | | | | |
| Post-processing: Minimum Match 0% | | | | | | | | | | | |
| Maximum Match 100% | | | | | | | | | | | |
| Listing first 45 summaries | | | | | | | | | | | |
| Database : EST:* | | | | | | | | | | | |
| 1: em_estba:* | | | | | | | | | | | |
| 2: em_estthum:* | | | | | | | | | | | |
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| 11: gb_htc:* | | | | | | | | | | | |
| 12: gb_gss:* | | | | | | | | | | | |
| 13: em_gss_hum:* | | | | | | | | | | | |
| 14: em_gss_inv:* | | | | | | | | | | | |
| 15: em_gss_pln:* | | | | | | | | | | | |
| 16: em_gss_vrt:* | | | | | | | | | | | |
| SUMMARIES | | | | | | | | | | | |
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| 1 | 380 | 100.0 | 380 | 10 | W36511 | W36511 | RESULT | 1 | | | |
| 2 | 189.2 | 48.7 | 462 | 9 | AA760573 | AA760573 | LOCUS | | | | |
| 3 | 174.8 | 46.0 | 361 | 10 | W10508 | W10508 | DEFINITION | | | | |
| 4 | 151.4 | 39.8 | 553 | 10 | BR466248 | BR466248 | IMAGE:335369', similar to SWILOX2_HUMAN P18054 ARACHIDONATE 12-LIPOXYGENASE ; mRNA sequence. | | | | |
| 5 | 131.6 | 34.6 | 645 | 10 | BR436629 | BR436629 | ACCESSION | | | | |
| 6 | 121.6 | 32.0 | 325 | 10 | BR4946103 | BR4946103 | VERSION | | | | |
| 7 | 115.1 | 30.3 | 499 | 9 | AW488909 | AW488909 | KEYWORDS | | | | |
| 8 | 114.6 | 30.2 | 818 | 10 | BR6697813 | BR6697813 | EST. | | | | |
| 9 | 100.4 | 26.4 | 795 | 10 | BR1667266 | BR1667266 | SOURCE | | | | |
| 10 | 97.2 | 25.5 | 100 | 10 | W18678 | W18678 | ORGANISM | | | | |
| 11 | 93.4 | 24.6 | 518 | 9 | AW188059 | AW188059 | TITLE | | | | |
| 12 | 89.8 | 23.6 | 214 | 9 | BB587762 | BB587762 | JOURNAL | | | | |
| 13 | 88.0 | 23.2 | 214 | 9 | AA038641 | AA038641 | COMMENT | | | | |
| 14 | 80.4 | 21.2 | 257 | 9 | AA138542 | AA138542 | CONTACT: Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub回国que, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterson, R. | | | | |
| 15 | 80.4 | 21.2 | 449 | 9 | AA138542 | AA138542 | Unpublished (1996) | | | | |
| 16 | 75.5 | 19.7 | 277 | 10 | BB715737 | BB715737 | The Wasu-HIM Mouse EST Project | | | | |
| 17 | 66.4 | 17.5 | 445 | 10 | BF464406 | BF464406 | Contact: Marra, M. Mouse EST Project | | | | |
| FEATURES | | | | | | | | | | | |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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 TGTGACCATCGAGGAGCGGCCATTTTTTTTTTTTTTTT 3'],
 double stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pNT3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento

Washington University School of Medicine[®]
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LBNL; co-
IMAGE Consortium (info@image.lnl.gov) for further info
MGI:1654157
Possible reversed clone: similarity on wrong strand
Seq. Primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 357.

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through
IMAGE Consortium (info@image.llnl.gov)
MGI:654157
Possible reversed clone: similarity on
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 357.

hrough LLNL
for further
am
wrong stran

nd ; contact the
r information.

Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University).^a

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FEATURES          Location/Qualifiers
Source           1. .462
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Locus AA760573 **Version** 462 **bp** **mRNA** **Definition** linear EST 23-JAN-1991
Accession VV78603 **Source** r1. Stratagene mouse skin (#937313) **Mus musculus** cDNA clone
Image AA122855 5, similar to SWILOX2_HUMAN P188054 ARACHIDONATE 12-LIPOXGENASE ; mRNA sequence.
Keywords AA760573, RA760573.1, GI:2808367
Organism Mus musculus
Title house mouse
Journal Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Author Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Reference 1 (bases 1 to 462)
Authors Marra, M., Hillier, L., Alien, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Stettloe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
Comment The WashU-HMM Mouse EST Project
Unpublished Unpublished (1996)
Contact Contact: Marra M/Mouse EST Project
Project WashU-HMM Mouse EST Project

| | |
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| RESULT | W10508 |
| LOCUS | W10508 |
| DEFINITION | 361 bp mRNA linear EST 01-OCT-1997 |
| IMAGE | ma40646.rl Soares mouse p3MFI.5 Mus musculus cDNA clone |
| 5-LIPOXYGENASE | IMAGE:3131875, similar to SW:LOX5_RAT p12527 ARACHIDONATE mRNA sequence. |
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| VERSION | W10508.1 |
| KEYWORDS | GI:1204834 |
| SOURCE | EST. |
| ORGANISM | house mouse. |
| MUS | musculus |
| Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | |
| REFERENCE | 1 (bases 1 to 361) |
| AUTHORS | Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubroque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. |
| TITLE | The WashU-HMM Mouse EST Project |

| TITLE | | JOURNAL | |
|---|--------------------|---|---------------|
| COMMENT | | MEDLINE | |
| National Institutes of Health, Mammalian Gene Collection (MGC) | Unpublished (1999) | Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) | sequence tags |
| Contact: Robert Strausberg, Ph.D. | | 202/2663 | JOURNAL |
| Email: cgbps@mail.nih.gov | | Contact: Simpson A.J.G. | COMMENT |
| Tissue Procurement: DCTD/DTR/Genzard | | Ludwig Institute for Cancer Genetics | |
| CDNA Library Preparation: Ling Hong/Rubin Laboratory | | Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil | |
| DNA Sequencing by: Incyte Genomics, Inc. | | Tel: +55-11-2704922 | |
| Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: | | Fax: +55-11-2707001 | |
| http://image.llnl.gov | | Email: asimpson@ludwig.org.br | |
| plate: ILMC1383 row: b column: 07 | | This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?L=M3&t2=M3-KT0050-080101-001-c03t3-2001-01-08&t4=1) | |
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| /lab_host="BiolB (phage resistant)" | | /clone_id="KT0050" | |
| /note="Organ: lung; Vector: pBR; Site_1: XbaI; Site_2: | | /dev_state="Adult" | |
| EcoRI; cDNA made by oligo-dT priming. Directionally cloned | | /note="Organ: bladder_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." | |
| into EcoRI/XbaI sites using the following 5' adaptor: GGAAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC library." | | BASE COUNT | |
| 122 a 201 c 190 g 132 t | | 77 a 99 c 155 g 94 t | |
| ORIGIN | | ORIGIN | |
| Query Match 34.6%; Score 131.6; DB 10; Length 645; | | Query Match 32.0%; Score 121.6; DB 10; Length 425; | |
| Best Local Similarity 80.6%; Pred. No. 5.7e-28; Mismatches 166; Conservative 0; Indels 1; Gaps 1; | | Best Local Similarity 82.0%; Pred. No. 4.1e-25; Mismatches 139; Conservative 0; Indels 0; Gaps 0; | |
| Db 175 TTTCCCTGGGCCCTAGAGGGCTCCACAGGTGATGGTCGGGCTGCTGAGCTTACCT 234 | | Db 175 TTTCCCTGGGCCCTAGAGGGCTCGCACAGGATGTCGGGCTGCTGAGCTCACC 234 | |
| Qy 425 TGTCTCTGGCGTGAAGCTTCTGGGTTGATGTTGAGCTGGGCTCAGCTGGAT 294 | | Qy 425 TGTCTCTGGGCCGGAGGCTTGCTGGGATGTTGAGCTGGGCTCAGCTGGAT 294 | |
| Db 235 ACAAAAGCCCTCTGCAATTCCCAACGACTTGTGGAGCCTGGGCTCAGGACCTGGAT 294 | | Db 235 ACAAAAGCCCTCTGCAATTCCCAACGACTTGTGGAGCCTGGGCTCAGGACCTGGAT 294 | |
| Qy 485 ATGACAGCCTCTACTCTCCCAATGACTTGTGGAGCCTGGGCTCAGGACCTGGAT 544 | | Qy 295 ATTATTCCTGATGACAGCTGGGCTCAGGACCTGGGCTCAGGACCTGGAT 354 | |
| Db 295 ATTATTCCTGATGACAGCTGGGCTCAGGACCTGGGCTCAGGACCTGGAT 354 | | Db 295 ATTATTCCTGATGACAGCTGGGCTCAGGACCTGGGCTCAGGACCTGGAT 342 | |
| Qy 545 ATTACTACCCGATGACAGCTGGGCTCAGGACCTGGGCTCAGGACCTGGAT 603 | | Qy 295 ATTATTCCTGATGACAGCTGGGCTCAGGACCTGGGCTCAGGACCTGGAT 342 | |
| Db 355 ATCATCACTTATTACCAATGAC 380 | | Db 604 ATCATCACTTATTACCCGGTGTAC 629 | |
| RESULT 6 | | RESULT 7 | |
| LOCUS BG946103 | | LOCUS AW88090/c | |
| DEFINITION 425 bp mRNA linear EST 11-JUN-2001 | | DEFINITION UI-M-BH3-arr-e-11-1-UI_s1_NIH_BMAP_M_S4 Mus musculus cDNA clone | |
| ACCESSION MR3-KT0050-080101-001-c03 | | ACCESSION UI-M-BH3-arr-e-11-0-UI_3'_mRNA sequence. | |
| VERSION BG946103 | | VERSION AW88090 | |
| VERSION BG346103.1 | | VERSION AW88090.1 | |
| VERSION GI:14345474 | | VERSION GI:7058360 | |
| KEYWORDS EST. | | KEYWORDS EST. | |
| SOURCE human. | | SOURCE house mouse. | |
| ORGANISM Homo sapiens | | ORGANISM Mus musculus | |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | |
| REFERENCE I (bases 1 to 425) | | REFERENCE 1 (bases 1 to 499) | |
| AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Negai, M.A., da Silva, W., Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldzman, G.H., Carvalho, A.F., Matsuoka, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J. | | AUTHORS Ronald, M.F., Lennon, G. and Soares, M.B. | |
| COMMENT shotgun sequencing of the human transcriptome with ORF expressed | | COMMENT Normalization and subtraction: two approaches to facilitate gene discovery | |
| JOURNAL Genes Res. 6 (9), 791-806 (1996) | | JOURNAL Genes Res. 6 (9), 791-806 (1996) | |
| MEDLINE 9704477 | | MEDLINE 9704477 | |
| COMMENT Contact: Chin, H | | COMMENT National Institute of Mental Health | |
| TITLE | | 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD | |

20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mbs@mail.nih.gov
 Oligo-dt track not found. Not 1 site shown in beginning of sequence
 is likely internal to the message. cDNA Library Preparation: M.B.
 Soares lab clone distribution: Researchers may obtain BMAP cDNA
 clones from RESEARCH GENETICS. It should be noted that Bento Soares
 is generating a small number of additional specialized
 non-redundant arrays of BMAP cDNAs whose availability will be
 considered under appropriate and limited collaborative arrangements
 Seq primer: M13 Forward
 POLY=A=NO.

FEATURES source

POLY=A=NO.

Location/Qualifiers

1. .499

/organism="Mus musculus"

/strain="C57Bl/6J"

/db_xref="taxon:10090"

/clone="01-MBH3-arr-e-11-0-01"

/dev_stage "27-32 days"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pTT3D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; The

NIH_BMAP_M_S4 library is a subtracted library of a series,

ultimately derived from a mixture of individually tagged

normalized libraries from ten regions of the mouse brain

(cerebellum, brain stem, olfactory bulbs, hypothalamus,

cortex, amygdala, basal ganglia, pineal gland, striatum,

hippocampus) after a series of subtractions to reduce the

representation of cDNAs from which ESTs had already been

generated. The following serially subtracted libraries

were generated in this process: NIH_BMAP_M_S4,

NIH_BMAP_M_S3_3, NIH_BMAP_M_S3_2, NIH_BMAP_M_S3_1,

NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library

(NIH_BMAP_M_S4) was constructed as follows: PCRamplified

cDNA inserts from NIH_BMAP_M_S3_3, NIH_BMAP_M_S3_2, and

NIH_BMAP_M_S3_1 clones from which 3' ESTs had been derived

the NIH_BMAP_M_S3_3, NIH_BMAP_M_S3_2, and NIH_BMAP_M_S3_1

libraries in the form of single-stranded circles. The

remaining single-stranded circles (subtracted library)

was purified by hydroxyapatite column chromatography,

converted to double-stranded circles and electroporated

into DH10B bacteria (LifeTechnologies) to generate the

NIH_BMAP_M_S4 library. This procedure has been previously

described (Bonaldo, Lennon and Soares, Genome Research

6, 791-806, 1996)

TAG_LIB=NIH_BMAP_M_S4

TAG_TISSUE=basal_ganglia

TAG_SEQ="TGATAC"

BASE COUNT

107 a 139 c 142 g 111 t

ORIGIN

Query Match

30.3%; Score 115; DB 9; Length 499;

Best Local Similarity 95.6%; Pred. No. 3; 8e-23;

Matches 129; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Query Match

30.2%; Score 114.6; DB 10; Length 818;

Best Local Similarity 75.6%; Pred. No. 6; 3e-23;

Matches 155; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

Query Match

175 TⁿCCCTCGGCTAGAGGGCTCGCACAGTGATGTTGGGGTGTAGCTCACC

Db 417 TGTCCCTGGGGTGGAGGCTTGTGTTGGGGTGTAGCTCACC

Query Match

235 ACAAAAGCCTCTGCACTCCAAAGC-ACTTGTGGAGGGGGTCAGGACACTGCCTGG

Db 477 ATGACAGCCTCTACCTCCCCATGCACCTTGTTGGAGCGCTGGCCAGGACTCTGG

Query Match

294 TATTATTCGGTGTACACGGCTGGGGTGGTACGGCATGGAGGTTACGTTACTGA

Db 537 TATTACTACCGCGATGACAGCTGGGGGGTGGGAATGCACTGGAGAGATATGTGACCGA

Query Match

354 GATCATCACTTATTTACCGAG 378

Db 597 GATCATCACTTATTTACCGAG 621

RESULT 9

B1667266

LOCUS B1667266

DEFINITION 60270308F1 NCL_CGAP_Skn3

mRNA sequence

LINEAR 818 bp

mRNA linear EST 07-MAY-2001

VERSION 1

KEYWORDS IMAGE:5311901 5,

EST B1667266.1 GI:15581499

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo.

COMMENT EST.

REFERENCE 1 (bases 1 to 818)

AUTHORS NIH-MGC

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-@email.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The T.M.A.G.E. Consortium (TLLN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the T.M.A.G.E. Consortium/TLLN at:

http://image.llnl.gov

Plate: LLNL010691 row: 0 column: 21

High quality sequence stop: 779.

Location/Qualifiers

1. .818

/organism="Homo sapiens"

/db_xref="taxon:9600"

/clone_1_id="NCL_CGAP_Skn3"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average Insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCL_CGAP Library."

ORIGIN

Query Match

30.2%; Score 114.6; DB 10; Length 818;

Best Local Similarity 75.6%; Pred. No. 6; 3e-23;

Matches 155; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

Query Match

175 TⁿCCCTCGGCTAGAGGGCTCGCACAGTGATGTTGGGGTGTAGCTCACC

Db 417 TGTCCCTGGGGTGGAGGCTTGTGTTGGGGTGTAGCTCACC

Query Match

235 ACAAAAGCCTCTGCACTCCAAAGC-ACTTGTGGAGGGGGTCAGGACACTGCCTGG

Db 477 ATGACAGCCTCTACCTCCCCATGCACCTTGTTGGAGCGCTGGCCAGGACTCTGG

Query Match

294 TATTATTCGGTGTACACGGCTGGGGTGGTACGGCATGGAGGTTACGTTACTGA

Db 537 TATTACTACCGCGATGACAGCTGGGGGGTGGGAATGCACTGGAGAGATATGTGACCGA

Query Match

354 GATCATCACTTATTTACCGAG 378

Db 597 GATCATCACTTATTTACCGAG 621

RESULT 9

B1667266

LOCUS B1667266

DEFINITION 60270308F1 NCL_CGAP_Skn3

mRNA sequence

LINEAR 818 bp

mRNA linear EST 07-MAY-2001

VERSION 1

KEYWORDS IMAGE:5311901 5,

EST B1667266.1 GI:15581499

SOURCE Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo.

COMMENT EST.

REFERENCE 1 (bases 1 to 818)

AUTHORS NIH-MGC

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-@email.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The T.M.A.G.E. Consortium (TLLN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the T.M.A.G.E. Consortium/TLLN at:

http://image.llnl.gov

Plate: LLNL010691 row: 0 column: 21

High quality sequence stop: 779.

Location/Qualifiers

1. .818

/organism="Homo sapiens"

/db_xref="taxon:9600"

/clone_1_id="NCL_CGAP_Skn3"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.

Average Insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCL_CGAP Library."

ORIGIN

Query Match

30.2%; Score 114.6; DB 10; Length 818;

Best Local Similarity 75.6%; Pred. No. 6; 3e-23;

Matches 155; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

Query Match

175 TⁿCCCTCGGCTAGAGGGCTCGCACAGTGATGTTGGGGTGTAGCTCACC

Db 417 TGTCCCTGGGGTGGAGGCTTGTGTTGGGGTGTAGCTCACC

Query Match

235 ACAAAAGCCTCTGCACTCCAAAGC-ACTTGTGGAGGGGGTCAGGACACTGCCTGG

Db 477 ATGACAGCCTCTACCTCCCCATGCACCTTGTTGGAGCGCTGGCCAGGACTCTGG

Query Match

294 TATTATTCGGTGTACACGGCTGGGGTGGTACGGCATGGAGGTTACGTTACTGA

Db 537 TATTACTACCGCGATGACAGCTGGGGGGTGGGAATGCACTGGAGAGATATGTGACCGA

Query Match

354 GATCATCACTTATTTACCGAG 378

Db 597 GATCATCACTTATTTACCGAG 621

RESULT 9

B1667266

LOCUS B1667266

DEFINITION 60270308F1 NCL_CGAP_Skn3

mRNA sequence

LINEAR 818 bp

mRNA linear EST 07-MAY-2001

VERSION 1

KEYWORDS IMAGE:5311901 5,

EST B1667266.1 GI:15581499

SOURCE Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo.

COMMENT EST.

REFERENCE 1 (bases 1 to 818)

AUTHORS NIH-MGC

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-@email.nih.gov

Tissue Procurement: James Cleaver, M.D.

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found through the T.M.A.G.E. Consortium/TLLN at:

http://image.llnl.gov

Plate: LLNL010691 row: 0 column: 21

High quality sequence stop: 779.

Location/Qualifiers

1. .818

/organism="Homo sapiens"

/db_xref="taxon:9600"

/clone_1_id="NCL_CGAP_Skn3"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.

Average Insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCL_CGAP Library."

ORIGIN

Query Match

30.2%; Score 114.6; DB 10; Length 818;

Best Local Similarity 75.6%; Pred. No. 6; 3e-23;

Matches 155; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

Query Match

175 TⁿCCCTCGGCTAGAGGGCTCGCACAGTGATGTTGGGGTGTAGCTCACC

Db 417 TGTCCCTGGGGTGGAGGCTTGTGTTGGGGTGTAGCTCACC

Query Match

235 ACAAAAGCCTCTGCACTCCAAAGC-ACTTGTGGAGGGGGTCAGGACACTGCCTGG

Db 477 ATGACAGCCTCTACCTCCCCATGCACCTTGTTGGAGCGCTGGCCAGGACTCTGG

Query Match

294 TATTATTCGGTGTACACGGCTGGGGTGGTACGGCATGGAGGTTACGTTACTGA

Db 537 TATTACTACCGCGATGACAGCTGGGGGGTGGGAATGCACTGGAGAGATATGTGACCGA

Query Match

354 GATCATCACTTATTTACCGAG 378

Db 597 GATCATCACTTATTTACCGAG 621

RESULT 9

B1667266

LOCUS B1667266

DEFINITION 60270308F1 NCL_CGAP_Skn3

mRNA sequence

LINEAR 818 bp

mRNA linear EST 07-MAY-2001

VERSION 1

KEYWORDS IMAGE:5311901 5,

EST B1667266.1 GI:15581499

SOURCE Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo.

COMMENT EST.

REFERENCE 1 (bases 1 to 818)

AUTHORS NIH-MGC

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

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found through the T.M.A.G.E. Consortium/TLLN at:

http://image.llnl.gov

Plate: LLNL010691 row: 0 column: 21

High quality sequence stop: 779.

Location/Qualifiers

1. .818

/organism="Homo sapiens"

/db_xref="taxon:9600"

/clone_1_id="NCL_CGAP_Skn3"

/lab_host="DH10B (T1 phage-resistant)"

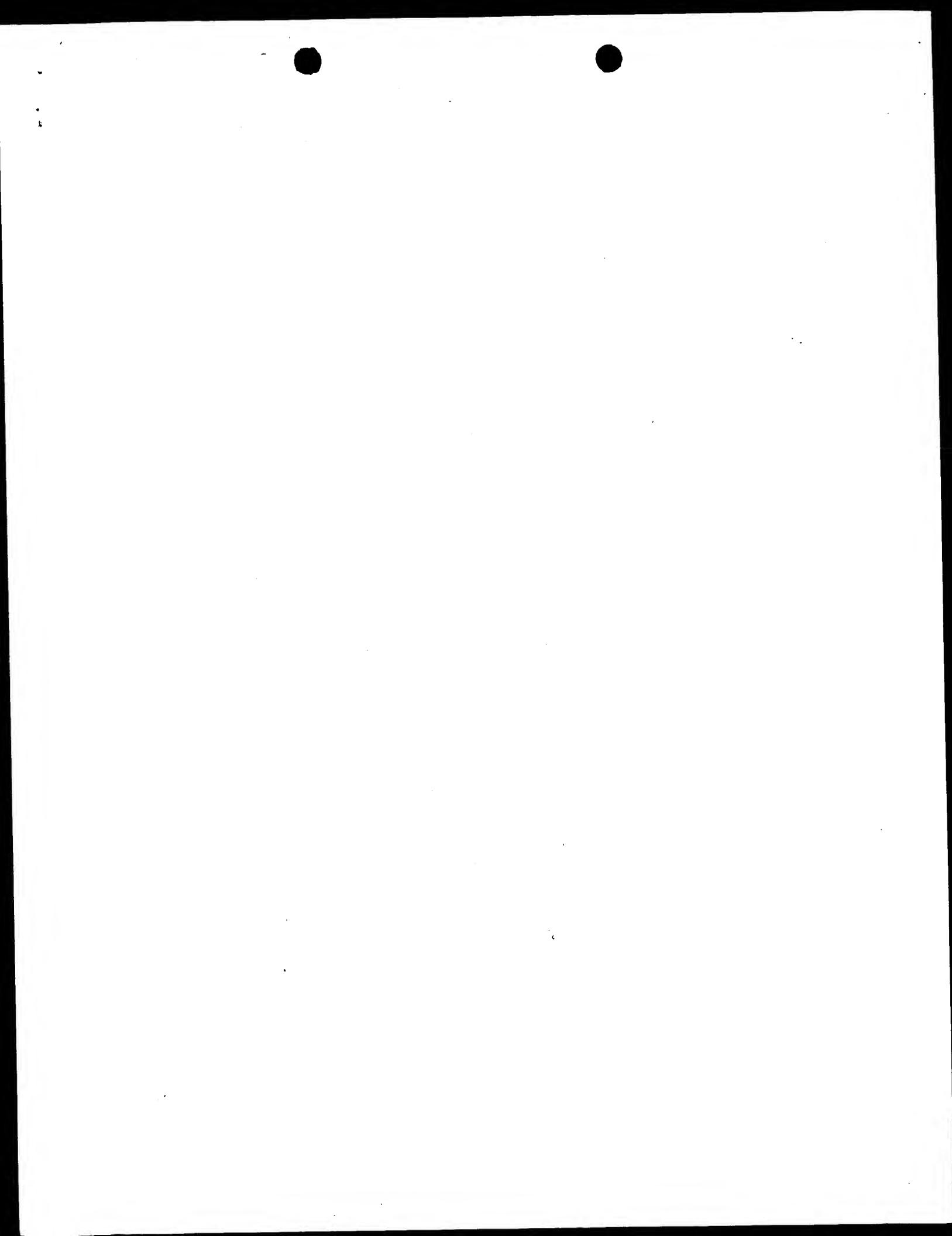
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Average Insert size 1.5kb. Library constructed by Life

| COMMENT | TITLE |
|--|--|
| Unpublished (1990) | The WashU-NCI Mouse EST Project 1999 |
| Contact: Marra M/WashU-NCI Mouse EST Project 1999 | WashU-HMI Mouse EST Project |
| Washington University School of Medicine | Washington University School of Medicine |
| 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA | 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 |
| Tel: 314 286 1800 | Tel: 314 286 1800 |
| Fax: 314 286 1810 | Fax: 314 286 1810 |
| Email: mouseest@atston.wustl.edu | Email: mouseest@wustl.edu |
| This clone is available royalty-free through LLNL; contact the | This clone is available royalty-free through LLNL; contact the |
| IMAGE Consortium (info@image.llnl.gov) for further information. | IMAGE Consortium (info@image.llnl.gov) for further information. |
| MGI: 995458 | MGI: 211595 |
| Seq primer: custom primer used | Possible reversed clone: similarity on wrong strand |
| High quality sequence stop: 518. | Seq primer: mob.REGATET |
| Location/Qualifiers | High quality sequence stop: 177. |
| 1. .518 | Location/Qualifiers |
| FEATURES | FEATURES |
| source | source |
| Query Match | Query Match |
| Best Local Similarity 98.9%; Pred. No. 8 7e-17; | Best Local Similarity 24.6%; Score 93.4; DB 9; Length 518; |
| Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |
| Db 12 | Db 12 |
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| 5'-LPOXYGENASE ;, mRNA sequence. | 1 gctgcgtccggctccagaggatccggggcagggttccggcttgactgtccatact 60 |
| VERSION W11802.1 | 72 |
| EST. | actgtcccaactcttccgttgccctcc 106 |
| BASE COUNT | 61 |
| ORIGIN | 61 gactgcgtccatcaactttcgtggcttcct 95 |
| RESULT 12 | RESULT 13 |
| LOCUS W11802 | LOCUS BB587762 |
| DEFINITION 214 bp mRNA Linear EST 02-OCT-1997 | DEFINITION BB587762 RIKEN full-length enriched adult female vagina mus |
| ACCESSION BB587762 | ACCESSION BB587762.1 |
| VERSION G1:11484306 | VERSION G1:11484306 |
| KEYWORDS EST. | KEYWORDS EST. |
| SOURCE house mouse. | SOURCE house mouse. |
| ORGANISM Mus musculus | ORGANISM Mus musculus |
| REFERENCE 1 (bases 1 to 214) | REFERENCE 1 (bases 1 to 214) |
| Aizawa, K., Akaihara, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., | Aizawa, K., Akaihara, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., |
| Hamagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y., | Hamagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y., |
| Imotani, K., Ishii, Y., Itoh, M., Irawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuya, T., Miyazaki, A., Nakamura, M., Nishi, K., | Imotani, K., Ishii, Y., Itoh, M., Irawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuya, T., Miyazaki, A., Nakamura, M., Nishi, K., |
| Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., | Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., |
| Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., | Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., |
| Thiesing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and | Thiesing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and |
| Waterson, R. | Waterson, R. |
| THE WashU-HMI Mouse EST Project | THE WashU-HMI Mouse EST Project |
| Unpublished (1996) | Unpublished (1996) |
| TITLE JOURNAL | TITLE RIKEN Mouse ESTS (Aizawa, K. et al. 2000) |

Search completed: May 25, 2002, 00:50:47
Job time: 24294 sec

Job time: 24294 sec



NAME/KEY: misc-feature
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 FEATURE:
 NAME/KEY: misc-feature

RESULT 6
 US-08-439-009A-3/c
 Sequence 3, Application US/08439009A
 ; Patent No. 604787
 ; GENERAL INFORMATION:
 ; APPLICANT: Donadio, S
 ; APPLICANT: Katz, L
 ; APPLICANT: McElpine, J B
 ; TITLE OF INVENTION: Method of Directing Biosynthesis of
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Steven F. Weinstock
 ; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
 ; STREET: Park Rd
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: US
 ; ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/439,009A
 FILING DATE: 11-MAY-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Casuto, Dianne
 REGISTRATION NUMBER: 40,943
 REFERENCE/DOCKET NUMBER: 4952.US.D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-938-3137
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20225 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Saccharopolyspora erythraea

STRAIN: NRRL 2348
 FEATURE: ;
 NAME/KEY: CDS
 LOCATION: 19..10722
 OTHER INFORMATION: /codon_start= 19
 OTHER INFORMATION: /function= "gene eryA"
 OTHER INFORMATION: /product= "eryA ORF2 encoding modules 3 & 4 for 6-deoxyerythronolide B"
 FEATURE: misc_feature
 LOCATION: 19..4740
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: module 3"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 97..1482
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 1693..2670
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: acyltransferase domain of module 3"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 3406..3921
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: beta-ketoreductase domain of module 3"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 4171..4428
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: acyl carrier domain of module 3"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 4471..10722
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: module 4"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 4471..5847
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: beta-ketoacyl ACP synthase domain of module 4"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 6054..7026
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: acyltransferase domain of module 4"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 7165..9216
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: dehydratase and enoylreductase domains in"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 9433..9984
 OTHER INFORMATION: /function= "approximate span
 OTHER INFORMATION: beta-ketoreductase of module 4"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 10225..10483
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: acyl carrier domain of module 4"
 FEATURE: ;
 NAME/KEY: CDS
 LOCATION: 10723..20235
 OTHER INFORMATION: /codon_start= 10723
 OTHER INFORMATION: /function= "gene eryA"
 OTHER INFORMATION: /product= "orf3 encoding modules 5 & 6"
 OTHER INFORMATION: 6-deoxyerythronolide B formation"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 10723..15165

FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 14062..14610
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: beta-ketoreductase of module 5"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 14857..15114
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: acyl carrier domain of module 5"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 15166..20235
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: acyltransferase domain of module 6"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 15172..15569
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: beta-ketoacyl ACP synthase domain of module 6"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 16768..17721
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: acyltransferase domain of module 6"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 18379..18921
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: beta-ketoreductase domain of module 6"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 19449..19398
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: acyl carrier domain of module 6"
 FEATURE: ;
 NAME/KEY: misc_feature
 LOCATION: 19492..20235
 OTHER INFORMATION: /function= "approximate span of
 OTHER INFORMATION: thioesterase domain of module 6"
 US-08-439-009A-3

Query Match 8.7%; Score 33.2; DB 3; Length 20235;
 Best Local Similarity 52.1%; Pred. No. 0.59; Mismatches 68; Indels 0; Gaps 0;

QY 189 GAGGGCTTCCACAGGTGATGGTTCGGGGCTCTCTGAGCTCACCTACAAAGCCCTGTC 248
 Db 17682 GAGCTCGCGATCAGGTGCTCCCGCGGTGACGCCGATGCCACGGC 17623
 QY 249 ATTCGCAACGACTTGTGAGCGGGGTCCAGACGCCCTGGGTTATTTCGTGAT 308
 Db 17622 GTCCCGGGATCTCTGACCCSCCGCGCTGAGCACGGTGGGGTCACTCGACGAA 17663
 QY 309 GACAGCTGCGGGTGGTACG 330
 Db 17562 GTGGCGTGAACGTCGGGACG 17541

US-09-099-749-10
 ; Sequence 10, Application US/09099749B
 ; Patent No. 6306591
 ; GENERAL INFORMATION:
 ; APPLICANT: Utah State University
 ; TITLE OF INVENTION: Screening For The Molecular Defect Causing Spider Lamb
 ; FILE REFERENCE: 3700US
 ; CURRENT APPLICATION NUMBER: US/09/099, 749B
 ; CURRENT FILING DATE: 1998-06-18
 ; EARLIER APPLICATION NUMBER: 60/050, 127
 ; EARLIER FILING DATE: 1991-06-18
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Corel Wordperfect 8.0
 ; SEQ ID NO: 10
 ; LENGTH: 2049
 ; TYPE: DNA
 ; ORGANISM: Sheep
 ; US-09-099-749-10

RESULT 8
 Query Match 8.5%; Score 32.4; DB 4; Length 2049;
 Best Local Similarity 55.3%; Pred. No. 0.34; Indels 51; Gaps 0;
 Matches 63; Conservative 0; Mismatches 0; Gaps 0;
 ; Sequence 1, Application US/08852806
 ; Patent No. 5874245
 ; GENERAL INFORMATION:
 ; APPLICANT: Shoji Fukusumi
 ; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Shuji Hinuma
 ; STREET: 709 Smedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19406-0939
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/852, 806
 ; FILING DATE: 16 MAY 1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Han, William T
 ; REGISTRATION NUMBER: 34, 344
 ; REFERENCE/DOCKET NUMBER: TAK50002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0700
 ; TELELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3271 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; US-08-852-806-1

RESULT 9
 Query Match 8.1%; Score 30.8; DB 2; Length 3271;
 Best Local Similarity 66.7%; Pred. No. 1.5; Indels 22; Gaps 0;
 Matches 44; Conservative 0; Mismatches 0; Gaps 0;
 ; Sequence 1, Application US/09163669
 ; Patent No. 611076
 ; GENERAL INFORMATION:
 ; APPLICANT: FUJIMI, SHUJI
 ; APPLICANT: HINUMA, SHUJI
 ; APPLICANT: FUJII, RYO
 ; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR (HIBC07)
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ratner & Prestia
 ; STREET: P.O. Box 980
 ; CITY: Valley Forge
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/163, 669
 ; FILING DATE: 30-SEP-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/852, 806
 ; FILING DATE: 07-MAY-1997
 ; APPLICATION NUMBER: 60/017, 915
 ; FILING DATE: 16-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Prestia, Paul F
 ; REGISTRATION NUMBER: 23, 031
 ; REFERENCE/DOCKET NUMBER: TAK-50002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0700
 ; TELELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3271 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-163-669-1

RESULT 10
 Query Match 8.1%; Score 30.8; DB 2; Length 3271;
 Best Local Similarity 66.7%; Pred. No. 1.5; Indels 22; Gaps 0;
 Matches 44; Conservative 0; Mismatches 0; Gaps 0;
 ; Sequence 1, Application US/09163669
 ; Patent No. 611076
 ; GENERAL INFORMATION:
 ; APPLICANT: FUJIMI, SHUJI
 ; APPLICANT: HINUMA, SHUJI
 ; APPLICANT: FUJII, RYO
 ; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR (HIBC07)
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ratner & Prestia
 ; STREET: P.O. Box 980
 ; CITY: Valley Forge
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/163, 669
 ; FILING DATE: 30-SEP-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/852, 806
 ; FILING DATE: 07-MAY-1997
 ; APPLICATION NUMBER: 60/017, 915
 ; FILING DATE: 16-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Prestia, Paul F
 ; REGISTRATION NUMBER: 23, 031
 ; REFERENCE/DOCKET NUMBER: TAK-50002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0700
 ; TELELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3271 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-163-669-1

Query Match 8.1%; Score 30.8; DB 3; length 3271;
 Best Local Similarity 66.7%; Pred. No. 1.5;
 Matches 44; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 4 AGGCAGCAGCTGGTCCCCGCTCCAGAGGCAATCGCGGAGACTGGGTTCCCGCTRACTGCT 63
 Db 239 AGACAGCGGCGGTGGCAGACCTGAGGCACTGGGGCACTGTGTTAGATATCTCG 180

QY 64 CCCTCA 69
 Db 179 CCAGCA 174

RESULT 10
 - US-07-741-453A-62
 Sequence 62, Application US/07741453A
 ; Patent No. 6228597

GENERAL INFORMATION:
 APPLICANT: PARMENTIER, MARC
 APPLICANT: LIBERT, FREDERIC
 APPLICANT: DUMONT, JACQUES
 APPLICANT: VASSART, GILBERT
 TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
 TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTEORS
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 STREET: 1615 L STREET, N.W.
 CITY: WASHINGTON, D.C.
 COUNTRY: U.S.A.
 ZIP: 20036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07-741,453A
 FILING DATE: 19911015
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16773
 REFERENCE/DOCKET NUMBER: 911913/1107/US/ST

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 861-3000
 TELEFAX: (202) 861-0944
 TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3710 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: cDNA
 ; US-07-741-453A-62

Query Match 7.9%; Score 30; DB 4; Length 3710;
 Best Local Similarity 49.4%; Pred. No. 3; Mismatches 0; Indels 0; Gaps 0;
 Matches 78; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 46 TGGTCCCGCTGACTCTCCATCACTGACGCTCCATCACTCTGGCTGCTGCTTC 105
 Db 126 TGGCTTCGCCCTGGGCGCTGCCCTTGCCCTTGCCCTTGACCCCTGAGATGGCTCTCAGTT 185

QY 106 TGCTTACCAAGCTGCTGCTCAGACTGATGTCGGAGGACTGGAGAGACTAAAGACAT 165
 Db 186 TGGCTCCACTGCTGCCGCTGAGGGAGGGCTGCTGGTGTACTGTAGTACTT 245

QY 166 TAAAGATATTTCCTGGGCTAGGGCTTCGACAG 203

Query Match 8.1%; Score 30.8; DB 1; Length 2297;
 Best Local Similarity 51.1%; Pred. No. 2.8; Mismatches 67; Indels 0; Gaps 0;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 TCCCTGGGCTGAGGCTCTGGAGGATGGGGTGGCTGGGGTGTGCTGAGCTACCTAC 236
 Db 272 TCCCTGGGCTGAGGATGGGGATACTGGTGTGAGGCTGCCAAATTGGACAACTGGATCC 331

QY 237 AAAAGCTCTCCATTCCACAGCTTGGAGACGGCGGGTCAAGAACCTGCTGGTAT 296
 Db 332 CAACAGCTCTTCAGATGGCTTGGGAGGGCTGCTGGTGTACTGTAGTACTT 391

QY 297 TATTCGGTGTAGACAG 313

RESULT 14

US-09-249-003-1

; Sequence 1, Application US/09249003

; Patent No. 6153188

; GENERAL INFORMATION:

; APPLICANT: Wilson, Peter J

; Morris, Charles P

; APPLICANT: Alison, Donald S

; APPLICANT: Occhiolino, Teresa

; APPLICANT: Blelicki, Julie

; APPLICANT: Clements, Peter R

; APPLICANT: Hopwood, John J

; TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF

; TITLE OF INVENTION: IDIOPRONE 2-SULFATASE

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Preaser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; APPLICATION NUMBER: US/09/249,003

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: DIGI910, Frank S

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 84162

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 516-742-4343

; TELEFAX: 516-742-4366

; TELEX: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2297 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE: CDS

; LOCATION: 125..1774

; US-09-249-003-1

Query Match 7.8%; Score 29.8; DB 3; Length 2297;
 Best Local Similarity 51.1%; Pred. No. 2.8;
 Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
 Qy 177 TCCCTGGCCCTAGAGGGCTCTGCAAGGGATGCTTCGGGTCTGAGCTCACCTAC 236
 Db 272 TCCCTGGCCCTAGAGGGATAAGCTGGTGGAGGCCAAATATTGACCAACTGGATCC 331
 Qy 237 AAAAGCTCTGATTCATGCCAACGACTTGTGGATGCCAGGGCTCTGGTCTGAGCTCACCTAC 296
 Db 332 CACAGCTCTCTGAGATGCTTGGCGAGGAGGTGTGGCCGAGCCGAGCCGGTT 391
 Qy 297 TATTCGGTGTGAGACAG 313
 Db 392 TCTTCCTCACTGGGAG 408

RESULT 15

US-08-726-214-7

; Sequence 7, Application US/08726214

; Patent No. 6107076

; GENERAL INFORMATION:

; APPLICANT: Tang, Wei-Jen

; NAME: Gilman, Alfred G.

; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/726,214

; FILING DATE: Concurrently Herewith

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/005,498

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/726,214

; FILING DATE: 04-OCT-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Highlander, Steven L.

; REGISTRATION NUMBER: 37,642

; REFERENCE/DOCKET NUMBER: US-08-450

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 471-7577

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3357 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

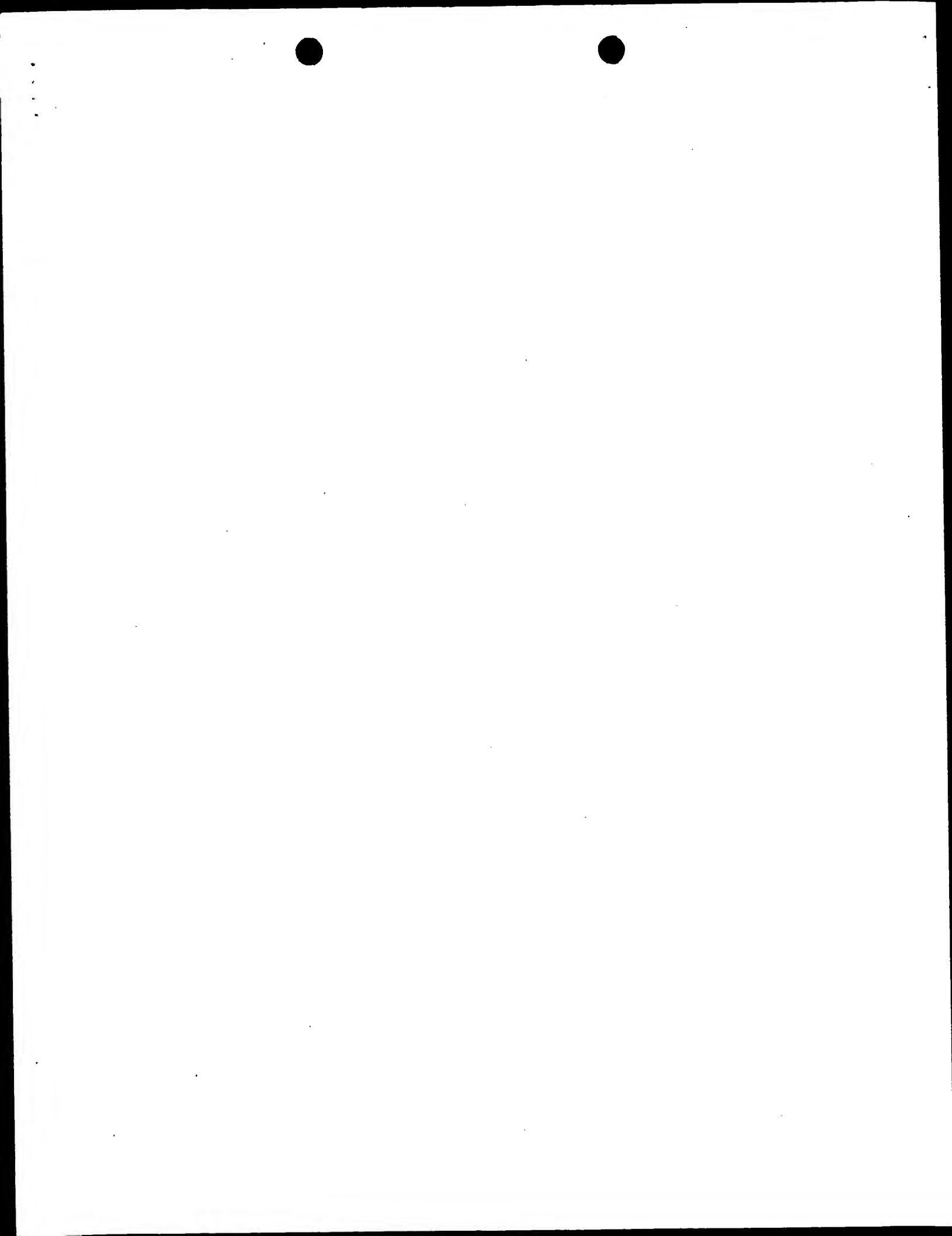
; TOPOLOGY: linear

; US-08-726-214-7

Query Match 7.8%; Score 29.8; DB 3; Length 3357;
 Best Local Similarity 50.3%; Pred. No. 3.3;
 Matches 73; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
 Qy 180 CTGGCTCTAGAGGGCTCTGCAACGACTTGTGGATGCCAGGGCTCTGGTCTGAGCTCACCTAC 239
 Db 962 CTGGCCAGTGGATGTTCCCTAAGGAGCAGTGTGCTCTAATGCTCATGAACCTCTGGCAA 1021
 Qy 240 AGCCCTGCAATTCCCAACGACTTGTGGACGGGGTCCAGGACCTCTGGTATTAT 299
 Db 1022 TTGGACCAAATGCAAGGAGCAGAATGCTGGATCCAGTCTGGAGACTGTAC 1081
 Qy 300 TTCCGTGATGACCTGGGGT 324
 Db 1082 TACTGTGATGCCGCTGCCCCCT 1106

; Search completed: May 25, 2002, 00:52:16

; Job time: 21553 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:

May 24, 2002, 23:55:26 ; Search time 315.63 Seconds

(without alignments)
2067.064 Million cell updates/sec

title:

W36511 1736436 seqs, 858457221 residues

perfect score:

380 1 GCAAGCCAGCAGCTCCC.....ACTTATTATTACAAATGAC 380

Sequence:

IDENTITY.NUC

Gapext 1.0

Scoring table:

20 Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802:*

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2: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1981.DAT:*

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4: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1983.DAT:*

5: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1984.DAT:*

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7: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1986.DAT:*

8: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1987.DAT:*

9: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1988.DAT:*

10: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1989.DAT:*

11: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1990.DAT:*

12: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1991.DAT:*

13: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1992.DAT:*

14: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1993.DAT:*

15: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1994.DAT:*

16: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1995.DAT:*

17: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1996.DAT:*

18: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1997.DAT:*

19: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1998.DAT:*

20: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1999.DAT:*

21: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA2000.DAT:*

22: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA2001.DAT:*

23: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.

Score

Match

Length

DB

ID

Description

1 135.8 35.7 2469 21 AAC55659

DNA encoding a hu

CDNA encoding a hu

FH OS
KEY Homo sapiens.
FT Location/Qualifiers
FT 1..2316
FT /*tag= a
FT /product= "lipoxygenase"
PN XX
XX WO20061765-A2.
PD XX
XX 19-OCT-2000.
PF XX
XX 12-APR-2000; 2000WO-US09657.
PR XX
XX 12-APR-1999; 99US-0128817.
PA XX
XX 24-AUG-1999; 99US-0150454.
PI XX
XX (LEXI-) LEXICON GENETICS INC.
PI Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;
XX WPI; 2000-665134/64.
PT P-PSDB; AAB19392.
PT Novel polynucleotides encoding human lipoxygenase proteins useful for
PT producing transgenic animals preferably mouse
PS XX
CC AAC61747-60 encode novel human lipoxygenase proteins. Lipoxygenases
CC oxidise lipids to produce leukotrienes. Leukotrienes bind cognate
CC receptors and trigger biological effects. Leukotrienes influence a
CC variety of biological processes, and can serve as, inter alia, potent
CC chemotactic agents and mediators of inflammation, smooth muscle
CC contractions, etc. Lipoxygenases and leukotrienes are implicated in
CC a variety of diseases and disorders, such as asthma, eye diseases,
CC arthritis, lung disease, cancer, acne, psoriasis, etc..
SQ Sequence 2316 BP; 486 A; 724 C; 651 G; 455 T; 0 other;

Query Match 14..58; Score 55..2; DB 21; Length 2316;
Best Local Similarity 54..4%; **Pred.** No. 1..3e-07;
Matches 111; **Conservative** 0; **Mismatches** 93; **Indels** 0; **Gaps** 0;
Qy 177 TCCCTGGCCTAGAGGCCTGGCAGGAGATGGTGGGGCTGTGTGAGCTACCTAC 236
Db 1867 tcacatggggcaggccatctatccatggacacggccgtggccacttcacctac 1925
Qy 237 AAACCTCTGATCCACAGCTTGTGGGGTCCAGGACCTGCGCTGGT 296
Db 1927 accaaatttcgtccgtccggacacgtccgtggccggccgtccgtatccacctac 1986
Qy 297 TATTCGCGATGAGCAGCTGGGGTGGTACGGATGGAGGTACGTAGAGAT 356
Db 1987 cactacccggagacggccgtggatctggggccatggagatctggatccgtggatcc 2046
Qy 357 CATACTTATTTACCAATGC 380
Db 2047 gtggggctacttattcccaatgtac 2070

RESULT 8
ID AAC61758
ID AAC61758 standard; cDNA; 2604 BP.
XX
AC AAC61758;
XX
DT 06-MAR-2001 (first entry)
DE cDNA encoding a human lipoxygenase protein.
XX
KW Human; lipoxygenase; leukotriene; lipid; chemotactic agent;
KW inflammation; smooth muscle contraction; asthma; eye disease; arthritis;
KW lung disease; cancer; acne; psoriasis; ss.

RESULT 9
ID AAC61747
ID AAC61747 standard; cDNA; 2701 BP.
AC AAC61747;
XX
DT 06-MAR-2001 (first entry)
DE cDNA encoding a human lipoxygenase protein.
XX
KW Human; lipoxygenase; leukotriene; lipid; chemotactic agent;
KW inflammation; smooth muscle contraction; asthma; eye disease; arthritis;

| | | | | |
|-----------------------|--------|--------------|----------|----------------|
| Query Match | 11.7% | Score 44.6; | DB 21; | Length 2343; |
| Best Local Similarity | 51.38% | Pred. No. | 0.00039; | |
| Matches | 101; | Conservative | 1; | Mismatches 95; |

aps 0;

RESULT 15
ID AAC58018
XX AAC58018 standard; DNA; 2343 BP.
AC AAC58018;
25-JAN-2001 (first entry)

Db 1480 ctcttctaccaraggg 1496

Search completed: May 25, 2002, 01:31:09
Job time: 5743 sec

Human; biallelic marker; arachidonic acid metabolism; genotyping; detection; hybridisation; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; identification; ERK; 12-LO-RBM; eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds

17-AUG-2000

11-FEB-2000; 2000W0-1B00184.
12-FEB-1999; 99US-0119917.
23-MAR-1999; 99US-0275257.
07-MAY-1999; 99US-0133200.
(GEST) GENSET.
Blumenfeld M, Bougueret L
WPI; 2000-5718815-3.
P-PSDB; AAB24019.

novel bimalleic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism -

The present invention describes polynucleotides including biallelic markers derived from genes involved in arachidonic acid metabolism and from genomic regions flanking those genes. Methods from the present invention may be used to select individuals for clinical trials and predict responses to treatment with drugs. The polynucleotides may be used in hybridisation assays, sequencing assays and specific amplification assays for identifying an elcosanoid-related biallelic marker (ERBM) or 12-LT-related biallelic marker, and for amplifying a segment of nucleotides containing an ERBM. The polynucleotides are useful in diagnostic kits. The markers may be used to detect conditions and genotypes associated with arachidonic acid metabolism. AAI57367 to AAC3018 and AAB24019 and AAB24020 represent sequences used in the exemplification of the present invention.

N.B. Polymorphic bases (single nucleotide polymorphisms also known as SNPs) in the polynucleotide sequences from the present invention have been given as their corresponding degenerate bases e.g. a polymorphic base of C or T has been given as Y.

Sequence 2343 BP; 511 A; 688 C; 636 G; 495 T; 13 other;

